

ABSTRACT

The present invention is directed to materials and methods for the identification and analysis of intermediate tandem repeat sequences in DNA, wherein an intermediate tandem repeat (ITR) sequence is a region of a DNA sequence containing at least one five to seven base repeat unit appearing in tandem at least two times. DNA markers to highly polymorphic ITR loci in the human genome are identified and analyzed, using particularly preferred embodiments of the materials and methods of the present invention.

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